

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/598,982C
Source: IFW16
Date Processed by STIC: 8/10/05

ENTERED

edit authorized by J.E. C. Low

**CRF Errors Edited by the STIC Systems
Branch**

Serial Number: 09/598,982C

CRF Edit Date: 8/10/05
Edited by: LR

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

✓ Other: converted submitted file to a generated
Patent In sequence listing



IFW16

RAW SEQUENCE LISTING DATE: 08/10/2005
 PATENT APPLICATION: US/09/598,982C TIME: 10:50:00

Input Set : A:\34506104.ST25.txt
 Output Set: N:\CRF4\08102005\I598982C.raw

3 <110> APPLICANT: Niles, Andrew
 4 Maffitt, Mark
 5 Haak-Frendscho, Mary
 7 <120> TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TRYPTASES, ACTIVE SITE MUTANTS
 THEREOF,
 8 AND METHODS OF MAKING SAME
 10 <130> FILE REFERENCE: 34506.104
 12 <140> CURRENT APPLICATION NUMBER: 09/598,982C
 13 <141> CURRENT FILING DATE: 2000-06-21
 15 <150> PRIOR APPLICATION NUMBER: 09/079,970
 16 <151> PRIOR FILING DATE: 1998-04-15
 18 <160> NUMBER OF SEQ ID NOS: 52
 20 <170> SOFTWARE: PatentIn version 3.3
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 735
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)..(735)
 32 <400> SEQUENCE: 1
 33 atc gtc ggg ggt cag gag gcc ccc agg agc aag tgg ccc tgg cag gtg 48
 34 Ile Val Gly Gly Gln Glu Ala Pro Arg Ser Lys Trp Pro Trp Gln Val
 35 1 5 10 15
 37 agc ctg aga gtc cac ggc cca tac tgg atg cac ttc tgc ggg ggc tcc 96
 38 Ser Leu Arg Val His Gly Pro Tyr Trp Met His Phe Cys Gly Gly Ser
 39 20 25 30
 41 ctc atc cac ccc cag tgg gtg ctg acc gca gcg cac tgc gtg gga ccg 144
 42 Leu Ile His Pro Gln Trp Val Leu Thr Ala Ala His Cys Val Gly Pro
 43 35 40 45
 45 gac gtc aag gat ctg gcc gcc ctc agg gtg caa ctg cgg gag cag cac 192
 46 Asp Val Lys Asp Leu Ala Ala Leu Arg Val Gln Leu Arg Glu Gln His
 47 50 55 60
 49 ctc tac tac cag gac cag ctg ctg ccg gtc agc agg atc atc gtg cac 240
 50 Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg Ile Ile Val His
 51 65 70 75 80
 53 cca cag ttc tac acc gcc cag atc gga gcg gac atc gcc ctg ctg gag 288
 54 Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile Ala Leu Leu Glu
 55 85 90 95
 57 ctg gag gag ccg gtg aac gtc tcc agc cac gtc cac acg gtc acc ctg 336
 58 Leu Glu Glu Pro Val Asn Val Ser Ser His Val His Thr Val Thr Leu
 59 100 105 110
 61 ccc cct gcc tca gag acc ttc ccc ccg ggg atg ccg tgc tgg gtc act 384
 62 Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly Met Pro Cys Trp Val Thr

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63          115          120          125
65 ggc tgg ggc gat gtg gac aat gat gag cgc ctc cca ccg cca ttt cct      432
66 Gly Trp Gly Asp Val Asp Asn Asp Glu Arg Leu Pro Pro Pro Phe Pro
67      130          135          140
69 ctg aag cag gtg aag gtc ccc ata atg gaa aac cac att tgt gac gca      480
70 Leu Lys Gln Val Lys Val Pro Ile Met Glu Asn His Ile Cys Asp Ala
71 145          150          155          160
73 aaa tac cac ctt ggc gcc tac acg gga gac gac gtc cgc atc gtc cgt      528
74 Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp Asp Val Arg Ile Val Arg
75          165          170          175
77 gac gac atg ctg tgt gcc ggg aac acc cgg agg gac tca tgc cag ggc      576
78 Asp Asp Met Leu Cys Ala Gly Asn Thr Arg Arg Asp Ser Cys Gln Gly
79          180          185          190
81 gac tcc gga ggg ccc ctg gtg tgc aag gtg aat ggc acc tgg ctg cag      624
82 Asp Ser Gly Gly Pro Leu Val Cys Lys Val Asn Gly Thr Trp Leu Gln
83      195          200          205
85 gcg ggc gtg gtc agc tgg ggc gag ggc tgt gcc cag ccc aac cgg cct      672
86 Ala Gly Val Val Ser Trp Gly Glu Gly Cys Ala Gln Pro Asn Arg Pro
87      210          215          220
89 ggc atc tac acc cgt gtc acc tac tac ttg gac tgg atc cac cac tat      720
90 Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp Ile His His Tyr
91 225          230          235          240
93 gtc ccc aaa aag ccg      735
94 Val Pro Lys Lys Pro
95          245
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 245
100 <212> TYPE: PRT
101 <213> ORGANISM: Homo sapiens
103 <400> SEQUENCE: 2
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106 1          5          10          15
109 Ser Leu Arg Val His Gly Pro Tyr Trp Met His Phe Cys Gly Gly Ser
110          20          25          30
113 Leu Ile His Pro Gln Trp Val Leu Thr Ala Ala His Cys Val Gly Pro
114          35          40          45
117 Asp Val Lys Asp Leu Ala Ala Leu Arg Val Gln Leu Arg Glu Gln His
118 50          55          60
121 Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg Ile Ile Val His
122 65          70          75          80
125 Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile Ala Leu Leu Glu
126          85          90          95
129 Leu Glu Glu Pro Val Asn Val Ser Ser His Val His Thr Val Thr Leu
130          100          105          110
133 Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly Met Pro Cys Trp Val Thr
134          115          120          125
137 Gly Trp Gly Asp Val Asp Asn Asp Glu Arg Leu Pro Pro Pro Phe Pro
138 130          135          140
141 Leu Lys Gln Val Lys Val Pro Ile Met Glu Asn His Ile Cys Asp Ala

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142 145          150          155          160
145 Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp Asp Val Arg Ile Val Arg
146          165          170          175
149 Asp Asp Met Leu Cys Ala Gly Asn Thr Arg Arg Asp Ser Cys Gln Gly
150          180          185          190
153 Asp Ser Gly Gly Pro Leu Val Cys Lys Val Asn Gly Thr Trp Leu Gln
154          195          200          205
157 Ala Gly Val Val Ser Trp Gly Glu Gly Cys Ala Gln Pro Asn Arg Pro
158          210          215          220
161 Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp Ile His His Tyr
162 225          230          235          240
165 Val Pro Lys Lys Pro
166          245
169 <210> SEQ ID NO: 3
170 <211> LENGTH: 40
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: PCR primer
177 <400> SEQUENCE: 3
178 gggcccctcg agaaaagaat cgtcgggggt caggaggccc          40
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 40
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: PCR primer
189 <400> SEQUENCE: 4
190 ccactatgtc cccaaaaagc cgtgaagcgg ccgccgctcg          40
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 771
195 <212> TYPE: DNA
196 <213> ORGANISM: Homo sapiens
199 <220> FEATURE:
200 <221> NAME/KEY: CDS
201 <222> LOCATION: (7)..(753)
203 <400> SEQUENCE: 5
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206          1          5          10
208 aag tgg ccc tgg cag gtg agc ctg aga gtc cac ggc cca tac tgg atg          96
209 Lys Trp Pro Trp Gln Val Ser Leu Arg Val His Gly Pro Tyr Trp Met
210 15          20          25          30
212 cac ttc tgc ggg ggc tcc ctc atc cac ccc cag tgg gtg ctg acc gca          144
213 His Phe Cys Gly Gly Ser Leu Ile His Pro Gln Trp Val Leu Thr Ala
214          35          40          45
216 gcg cac tgc gtg gga ccg gac gtc aag gat ctg gcc gcc ctc agg gtg          192
217 Ala His Cys Val Gly Pro Asp Val Lys Asp Leu Ala Ala Leu Arg Val
218          50          55          60

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220  caa ctg cgg gag cag cac ctc tac tac cag gac cag ctg ctg ccg gtc      240
221  Gln Leu Arg Glu Gln His Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val
222      65              70              75
224  agc agg atc atc gtg cac cca cag ttc tac acc gcc cag atc gga gcg      288
225  Ser Arg Ile Ile Val His Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala
226      80              85              90
228  gac atc gcc ctg ctg gag ctg gag gag ccg gtg aac gtc tcc agc cac      336
229  Asp Ile Ala Leu Leu Glu Leu Glu Glu Pro Val Asn Val Ser Ser His
230  95              100              105              110
232  gtc cac acg gtc acc ctg ccc cct gcc tca gag acc ttc ccc ccg ggg      384
233  Val His Thr Val Thr Leu Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly
234      115              120              125
236  atg ccg tgc tgg gtc act ggc tgg ggc gat gtg gac aat gat gag cgc      432
237  Met Pro Cys Trp Val Thr Gly Trp Gly Asp Val Asp Asn Asp Glu Arg
238      130              135              140
240  ctc cca ccg cca ttt cct ctg aag cag gtg aag gtc ccc ata atg gaa      480
241  Leu Pro Pro Pro Phe Pro Leu Lys Gln Val Lys Val Pro Ile Met Glu
242      145              150              155
244  aac cac att tgt gac gca aaa tac cac ctt ggc gcc tac acg gga gac      528
245  Asn His Ile Cys Asp Ala Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp
246      160              165              170
248  gac gtc cgc atc gtc cgt gac gac atg ctg tgt gcc ggg aac acc cgg      576
249  Asp Val Arg Ile Val Arg Asp Asp Met Leu Cys Ala Gly Asn Thr Arg
250  175              180              185              190
252  agg gac tca tgc cag ggc gac tcc gga ggg ccc ctg gtg tgc aag gtg      624
253  Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Val
254      195              200              205
256  aat ggc acc tgg ctg cag gcg ggc gtg gtc agc tgg ggc gag ggc tgt      672
257  Asn Gly Thr Trp Leu Gln Ala Gly Val Val Ser Trp Gly Glu Gly Cys
258      210              215              220
260  gcc cag ccc aac cgg cct ggc atc tac acc cgt gtc acc tac tac ttg      720
261  Ala Gln Pro Asn Arg Pro Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu
262      225              230              235
264  gac tgg atc cac cac tat gtc ccc aaa aag ccg tgaagcggcc gccgtcgt      771
265  Asp Trp Ile His His Tyr Val Pro Lys Lys Pro
266      240              245
269 <210> SEQ ID NO: 6
270 <211> LENGTH: 249
271 <212> TYPE: PRT
272 <213> ORGANISM: Homo sapiens
274 <400> SEQUENCE: 6
276  Leu Glu Lys Arg Ile Val Gly Gly Gln Glu Ala Pro Arg Ser Lys Trp
277  1              5              10              15
280  Pro Trp Gln Val Ser Leu Arg Val His Gly Pro Tyr Trp Met His Phe
281      20              25              30
284  Cys Gly Gly Ser Leu Ile His Pro Gln Trp Val Leu Thr Ala Ala His
285      35              40              45
288  Cys Val Gly Pro Asp Val Lys Asp Leu Ala Ala Leu Arg Val Gln Leu
289      50              55              60

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292 Arg Glu Gln His Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg
293 65                               70                               75                               80
296 Ile Ile Val His Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile
297                               85                               90                               95
300 Ala Leu Leu Glu Leu Glu Glu Pro Val Asn Val Ser Ser His Val His
301                               100                              105                              110
304 Thr Val Thr Leu Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly Met Pro
305                               115                              120                              125
308 Cys Trp Val Thr Gly Trp Gly Asp Val Asp Asn Asp Glu Arg Leu Pro
309                               130                              135                              140
312 Pro Pro Phe Pro Leu Lys Gln Val Lys Val Pro Ile Met Glu Asn His
313 145                               150                              155                              160
316 Ile Cys Asp Ala Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp Asp Val
317                               165                              170                              175
320 Arg Ile Val Arg Asp Asp Met Leu Cys Ala Gly Asn Thr Arg Arg Asp
321                               180                              185                              190
324 Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Val Asn Gly
325                               195                              200                              205
328 Thr Trp Leu Gln Ala Gly Val Val Ser Trp Gly Glu Gly Cys Ala Gln
329                               210                              215                              220
332 Pro Asn Arg Pro Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp
333 225                               230                              235                              240
336 Ile His His Tyr Val Pro Lys Lys Pro
337                               245
340 <210> SEQ ID NO: 7
341 <211> LENGTH: 27
342 <212> TYPE: DNA
343 <213> ORGANISM: Artificial Sequence
345 <220> FEATURE:
346 <223> OTHER INFORMATION: Mutagenesis oligonucleotide
348 <400> SEQUENCE: 7
349 gaggagccgg tgaaggtctc cagccac                                     27
352 <210> SEQ ID NO: 8
353 <211> LENGTH: 771
354 <212> TYPE: DNA
355 <213> ORGANISM: Homo sapiens
358 <220> FEATURE:
359 <221> NAME/KEY: CDS
360 <222> LOCATION: (7)..(753)
362 <400> SEQUENCE: 8
363 gggccc ctc gag aaa aga atc gtc ggg ggt cag gag gcc ccc agg agc   48
364      Leu Glu Lys Arg Ile Val Gly Gly Gln Glu Ala Pro Arg Ser
365      1           5           10
367 aag tgg ccc tgg cag gtg agc ctg aga gtc cac ggc cca tac tgg atg   96
368 Lys Trp Pro Trp Gln Val Ser Leu Arg Val His Gly Pro Tyr Trp Met
369 15           20           25           30
371 cac ttc tgc ggg ggc tcc ctc atc cac ccc cag tgg gtg ctg acc gca   144
372 His Phe Cys Gly Gly Ser Leu Ile His Pro Gln Trp Val Leu Thr Ala
373           35           40           45

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VERIFICATION SUMMARY

DATE: 08/10/2005

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**Raw Sequence Listing before editing,
for reference only**

09/598,982C

yy□□□□Project□□□□yy□□

(sample of submitted file)

**Does Not Comply
Corrected Diskette Needed**